

RAW SEQUENCE LISTING

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Application Serial Number: 10/558, 279
Source: PCT
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/558,279

DATE: 12/05/2005

TIME: 10:55:20

Input Set : A:\Sequence Listing ASCII, Docket No. 1700.0640000.ST25.txt
 Output Set: N:\CRF4\12052005\J558279.raw

3 <110> APPLICANT: Beerli, Roger R.
 4 Bachmann, Martin F.
 6 <120> TITLE OF INVENTION: Modified Polypeptides For Targeting Cell-Entry of the
 Adenoviruses of
 7 Subtype B
 9 <130> FILE REFERENCE: 1700.0640000/BJD/WBC
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/558,279
 C--> 11 <141> CURRENT FILING DATE: 2005-11-28
 11 <150> PRIOR APPLICATION NUMBER: EP03011184.3
 12 <151> PRIOR FILING DATE: 2003-05-27
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/005762
 15 <151> PRIOR FILING DATE: 2004-05-27
 17 <160> NUMBER OF SEQ ID NOS: 21
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1134
 22 <212> TYPE: DNA
 23 <213> ORGANISM: homo sapiens
 25 <400> SEQUENCE: 1

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30 tttgaagcta	tggagctcat	tggtaaacca	aaaccctact	atgagattgg	tgaacgagta	180
32 gattataagt	gtaaaaaagg	atacttctat	atacccctc	tgcaccacca	tactatttgt	240
34 gatcggaaatc	atacatggct	acctgtctca	gatgacgcct	gttatagaga	aacatgtcca	300
36 tatatacggg	atcctttaaa	tggccaagca	gtccctgcaa	atgggactta	cgagtttggt	360
38 tattcagatgc	actttatttg	taatgagggt	tattacttaa	ttgggtgaaga	aattctatat	420
40 tgtgaactta	aaggatcagt	agcaatttgg	agcggttaagc	ccccaatatg	tgaaaagggtt	480
42 ttgtgtacac	cacctccaaa	aataaaaaat	ggaaaaacaca	ccttttagtga	agtagaagta	540
44 tttagtatac	ttgatgcagt	aacttatagt	tgtgatcctg	cacctggacc	agatccattt	600
46 tcacttatttgc	gagagagcac	gatttattgt	ggtgacaatt	cagtgtggag	tcgtgctgct	660
48 ccagagtgtaa	aagtggctaa	atgtcgattt	ccagtagtcg	aaaatggaaa	acagatatca	720
50 ggatttggaa	aaaaatttta	ctacaaaagca	acagttatgt	ttgaatgcga	taagggtttt	780
52 tacctcgatg	gcagcgcacac	aattgtctgt	gacagtaaca	gtacttggga	tcccccaagtt	840
54 ccaaagtgtc	ttaaagtgtc	gacttcttcc	actacaaaat	ctccagcgtc	cagtgcctca	900
56 ggtccctaggc	ctacttacaa	gcctccagtc	tcaaattatc	caggatatcc	taaacctgag	960
58 gaaggaatac	ttgacagttt	ggatgtttgg	gtcattgctg	tgattgttat	tgccatagtt	1020
60 gttggagtttgc	cagtaatttg	tgttgcctcc	tacagatatc	ttcaaaggag	gaagaagaaaa	1080
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67 <212>	TYPE:	PRT				
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70 <220>	FEATURE:					
71 <221>	NAME/KEY:	SIGNAL				

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72 <222> LOCATION: (1)..(34)
73 <223> OTHER INFORMATION:
75 <220> FEATURE:
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77 <222> LOCATION: (35)..(328)
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86 <221> NAME/KEY: MISC_FEATURE
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88 <223> OTHER INFORMATION: SCR-1 domain
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93 <223> OTHER INFORMATION: SCR-2 domain
95 <220> FEATURE:
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97 <222> LOCATION: (161)..(224)
98 <223> OTHER INFORMATION: SCR-3 domain
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108 <223> OTHER INFORMATION: STP-B region
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111 <221> NAME/KEY: MISC_FEATURE
112 <222> LOCATION: (301)..(314).
113 <223> OTHER INFORMATION: STP-C region
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121 Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
122 20 25 30
125 Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
126 35 40 45
129 Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
130 50 55 60
133 Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
134 65 70 75 80
137 Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
138 85 90 95
141 Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
142 100 105 110

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145 Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
146 115 120 125
149 Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
150 130 135 140
153 Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
154 145 150 155 160
157 Leu Cys Thr Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
158 165 170 175
161 Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
162 180 185 190
165 Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
166 195 200 205
169 Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
170 210 215 220
173 Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
174 225 230 235 240
177 Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
178 245 250 255
181 Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
182 260 265 270
185 Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
186 275 280 285
189 Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro
190 290 295 300
193 Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
194 305 310 315 320
197 Glu Gly Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile Val
198 325 330 335
201 Ile Ala Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr Arg
202 340 345 350
205 Tyr Leu Gln Arg Arg Lys Lys Lys Gly Thr Tyr Leu Thr Asp Glu Thr
206 355 360 365
209 His Arg Glu Val Lys Phe Thr Ser Leu
210 370 375
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 15
215 <212> TYPE: PRT
216 <213> ORGANISM: artificial sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: polypeptide sequence of the STP-A region, which is inserted

before

220 e the STP-B region of CD46 in certain splice variants of CD46
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224 Val Leu Pro Pro Ser Ser Thr Lys Pro Pro Ala Leu Ser His Ser
225 1 5 10 15
228 <210> SEQ ID NO: 4
229 <211> LENGTH: 1110
230 <212> TYPE: DNA
231 <213> ORGANISM: homo sapiens
233 <400> SEQUENCE: 4

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236	ctggcgccca tggtgttgct gctgtactcc ttctccgatg cctgtgagga gccaccaaca	120
238	tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta	180
240	gattataagt gtaaaaaaagg atacttctat atacctcctc ttgccaccca tactatttgt	240
242	gatcggaaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca	300
244	tatatacggg atcctttaaa tggccaagca gtcctgcaa atgggactta cgagtttgg	360
246	tatcagatgc actttatttg taatgagggta tattacttaa ttgggtgaaga aattctatat	420
248	tgtgaactta aaggatcagt agcaatttgg agcggtaagc ccccaatatg tgaaaagggtt	480
250	tttgttacac cacctccaaa aataaaaaat ggaaaacaca ccttagtga agtagaagta	540
252	ttttagtatac ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt	600
254	tcacttattt gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct	660
256	ccagagtgtt aagtggtaaa atgtcgattt ccagtagtcg aaaatggaaa acagatata	720
258	ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt	780
260	tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt	840
262	ccaaagtgtc taaaagggtcc taggcctact tacaagcctc cagtctcaaa ttatccagga	900
264	tatcctaaac ctgaggaagg aataacttgc acgttggatg tttgggtcat tgctgtgatt	960
266	gttattgcca tagttgttgg agttgcagta atttgcgttgc tccctacag atatcttcaa	1020
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274	<211> LENGTH: 1089	
275	<212> TYPE: DNA	
276	<213> ORGANISM: homo sapiens	
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283	tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta	180
285	gattataagt gtaaaaaaagg atacttctat atacctcctc ttgccaccca tactatttgt	240
287	gatcggaaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca	300
289	tatatacggg atcctttaaa tggccaagca gtcctgcaa atgggactta cgagtttgg	360
291	tatcagatgc actttatttg taatgagggta tattacttaa ttgggtgaaga aattctatat	420
293	tgtgaactta aaggatcagt agcaatttgg agcggtaagc ccccaatatg tgaaaagggtt	480
295	tttgttacac cacctccaaa aataaaaaat ggaaaacaca ccttagtga agtagaagta	540
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299	tcacttattt gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct	660
301	ccagagtgtt aagtggtaaa atgtcgattt ccagtagtcg aaaatggaaa acagatata	720
303	ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt	780
305	tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt	840
307	ccaaagtgtc taaaagggtcc taggcctact tacaagcctc cagtctcaaa ttatccagga	900
309	tatcctaaac ctgaggaagg aataacttgc acgttggatg tttgggtcat tgctgtgatt	960
311	gttattgcca tagttgttgg agttgcagta atttgcgttgc tccctacag atatcttcaa	1020
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326	ctggcggcca	tggtgttgc	gctgtactcc	ttctccgatg	cctgtgagga	gccaccaaca	120
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330	gattataagt	gtaaaaaaagg	atacttctat	ataccccttc	ttgccacca	tactatttg	240
332	gatcggaaatc	atacatggct	acctgtctca	gatgacgcct	gttatagaga	aacatgtcca	300
334	tatatacggg	atccttaaaa	tggccaagca	gtccctgcaa	atgggactta	cgagtttggt	360
336	tatcagatgc	actttatgg	taatgaggg	tattacttaa	tttgtgaaga	aattctatat	420
338	tgtgaactta	aaggatcagt	agcaatttgg	agcgtaaagc	ccccaatatg	tgaaaagggtt	480
340	tttgttacac	cacccctaaaa	aataaaaaat	ggaaaacaca	ccttagtga	agtagaaagta	540
342	tttgagtatc	ttgatgcagt	aacttatagt	tgtgatcctg	cacctggacc	agatccattt	600
344	tcacttattt	gagagagcac	gatttattgt	ggtgacaatt	cagtgtggag	tcgtgctgct	660
346	ccagagtgt	aagtggtaaa	atgtcgattt	ccagtagtcg	aaaatggaaa	acagatata	720
348	ggattttggaa	aaaaatttta	ctacaaagca	acagttatgt	ttgaatgcga	taagggtttt	780
350	tacccatgt	gcagcgacac	aattgtctgt	gacagtaaca	gtacttgga	tccccagtt	840
352	ccaaagtgtc	ttaaagggtcc	taggcctact	tacaagctc	cagtctcaaa	ttatccagga	900
354	tatcctaaac	ctgaggaagg	aataacttgc	agttggatg	tttgggtcat	tgctgtgatt	960
356	gttattgcca	tagttgttgg	agttgcagta	atttgtgtt	tcccgtacag	atatcttcaa	1020
358	aggaggaaga	agaaaggaa	agcagatgtt	ggagctgaat	atgccactta	ccagactaaa	1080
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373	tttgaagcta	tggagctcat	tggtaaacca	aaaccctact	atgagatgg	tgaacgagta	180
375	gattataagt	gtaaaaaaagg	atacttctat	ataccccttc	ttgccacca	tactatttg	240
377	gatcggaaatc	atacatggct	acctgtctca	gatgacgcct	gttatagaga	aacatgtcca	300
379	tatatacggg	atccttaaaa	tggccaagca	gtccctgcaa	atgggactta	cgagtttggt	360
381	tatcagatgc	actttatgg	taatgaggg	tattacttaa	tttgtgaaga	aattctatat	420
383	tgtgaactta	aaggatcagt	agcaatttgg	agcgtaaagc	ccccaatatg	tgaaaagggtt	480
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389	tcacttattt	gagagagcac	gatttattgt	ggtgacaatt	cagtgtggag	tcgtgctgct	660
391	ccagagtgt	aagtggtaaa	atgtcgattt	ccagtagtcg	aaaatggaaa	acagatata	720
393	ggattttggaa	aaaaatttta	ctacaaagca	acagttatgt	ttgaatgcga	taagggtttt	780
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397	ccaaagtgtc	ttaaagggtcc	taggcctact	tacaagctc	cagtctcaaa	ttatccagga	900
399	tatcctaaac	ctgaggaagg	aataacttgc	agttggatg	tttgggtcat	tgctgtgatt	960
401	gttattgcca	tagttgttgg	agttgcagta	atttgtgtt	tcccgtacag	atatcttcaa	1020
403	aggaggaaga	agaaaggaa	agcagatgtt	ggagctgaat	atgccactta	ccagactaaa	1080
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416	ctggcggcca	tggtgttgc	gctgtactcc	ttctccgatg	cctgtgagga	gccaccaaca	120

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 35,1109

VERIFICATION SUMMARY DATE: 12/05/2005
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:80 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:73
L:90 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:83
L:560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1080